

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gregory, Richard J.
Wills, Ken N.
Maneval, Daniel C.
- (ii) TITLE OF INVENTION: Recombinant Adenoviral Vector and
Methods of Use
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Campbell and Flores
 - (B) STREET: 4370 La Jolla Village Drive, Suite 700
 - (C) CITY: San Diego
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 92122
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/328,673
 - (B) FILING DATE: 25-OCT-1994
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/233,777
 - (B) FILING DATE: 19-MAY-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/142,669
 - (B) FILING DATE: 25-OCT-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Campbell, Cathryn A.
 - (B) REGISTRATION NUMBER: 31,815
 - (C) REFERENCE/DOCKET NUMBER: P-CJ 1192
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (619) 535-9001
 - (B) TELEFAX: (619) 535-8949

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGCCACCGAG GGACCTGAGC GAGTC

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTCTGGGAAG GGACAGAAGA

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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGCGCTAGCT CTGCCCCAAA GAGCT

25

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGCGGTACCC TCGAGTCTAG ATATTGCCAG TGGTGAAG

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(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGTGCGGCCG CTGGAGGACT TTGAGGATGT CTGTC

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(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGCTCTAGAG AGACCAGTTA GGAAGTTTTC GCA

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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2995 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 139..2922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTGTAA CGGGAGTCGG GAGAGGACGG	60
GGCGTGCCCC GCGTGCGCGC GCGTCGTCTT CCCCCGCGCT CCTCCACAGC TCGCTGGCTC	120
CCGCCGCGGA AAGGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala 1 5 10	171
ACC GCC GCC GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro 15 20 25	219
CCT CCT GAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro 30 35 40	267
CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala 45 50 55	315
TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp 60 65 70 75	363
TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr 80 85 90	411
ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala 95 100 105	459
GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn 110 115 120	507

ATA Ile 125	GAA Glu 125	ATC Ile	AGT Ser	GTC Val	CAT His	AAA Lys 130	TTC Phe	TTT Phe	AAC Asn	TTA Leu 135	CTA Leu 135	AAA Lys	GAA Glu	ATT Ile	GAT Asp	555
ACC Thr 140	AGT Ser	ACC Thr	AAA Lys	GTT Val	GAT Asp 145	AAT Asn	GCT Ala	ATG Met	TCA Ser	AGA Arg 150	CTG Leu	TTG Leu	AAG Lys	AAG Lys	TAT Tyr 155	603
GAT Asp	GTA Val	TTG Leu	TTT Phe	GCA Ala 160	CTC Leu	TTC Phe	AGC Ser	AAA Lys	TTG Leu 165	GAA Glu	AGG Arg	ACA Thr	TGT Cys	GAA Glu 170	CTT Leu	651
ATA Ile	TAT Tyr	TTG Leu	ACA Thr 175	CAA Gln	CCC Pro	AGC Ser	AGT Ser	TCG Ser 180	ATA Ile	TCT Ser	ACT Thr	GAA Glu	ATA Ile 185	AAT Asn	TCT Ser	699
GCA Ala	TTG Leu	GTG Val 190	CTA Leu	AAA Lys	GTT Val	TCT Ser	TGG Trp 195	ATC Ile	ACA Thr	TTT Phe	TTA Leu 200	GCT Ala	AAA Lys	GGG Gly		747
GAA Glu 205	GTA Val	TTA Leu	CAA Gln	ATG Met	GAA Glu 210	GAT Asp	GAT Asp	CTG Leu	GTG Val	ATT Ile	TCA Ser 215	TTT Phe	CAG Gln	TTA Leu	ATG Met	795
CTA Leu 220	TGT Cys	GTC Val	CTT Leu	GAC Asp 225	TAT Tyr 225	TTT Phe	ATT Ile	AAA Lys	CTC Leu	TCA Ser 230	CCT Pro	CCC Pro	ATG Met	TTG Leu 235	CTC Leu 235	843
AAA Lys	GAA Glu	CCA Pro	TAT Tyr 240	AAA Lys	ACA Thr	GCT Ala	GTT Val	ATA Ile	CCC Pro 245	ATT Ile	AAT Asn	GGT Gly	TCA Ser	CCT Pro 250	CGA Arg	891
ACA Thr	CCC Pro	AGG Arg 255	CGA Arg	GGT Gly	CAG Gln	AAC Asn	AGG Arg	AGT Ser	GCA Ala 260	CGG Arg	ATA Ile	GCA Ala	AAA Lys 265	CAA Gln	CTA Leu	939
GAA Glu	AAT Asn 270	GAT Asp	ACA Thr	AGA Arg	ATT Ile	ATT Ile	GAA Glu 275	GTT Val	CTC Leu	TGT Cys	AAA Lys	GAA Glu 280	CAT His	GAA Glu	TGT Cys	987
AAT Asn 285	ATA Ile	GAT Asp	GAG Glu	GTG Val	AAA Lys	AAT Asn 290	GTT Val	TAT Tyr	TTC Phe	AAA Lys	AAT Asn 295	TTT Phe	ATA Ile	CCT Pro	TTT Phe	1035
ATG Met 300	AAT Asn	TCT Ser	CTT Leu	GGA Gly 305	CTT Leu	GTA Val	ACA Thr	TCT Ser	AAT Asn 310	GGA Gly	CTT Leu	CCA Pro	GAG Glu	GTT Val	GAA Glu 315	1083
AAT Asn	CTT Leu	TCT Ser	AAA Lys 320	CGA Arg	TAC Tyr	GAA Glu	GAA Glu	ATT Ile	TAT Tyr 325	CTT Leu	AAA Lys	AAT Asn	AAA Lys	GAT Asp 330	CTA Leu	1131
GAT Asp	GCA Ala	AGA Arg 335	TTA Leu	TTT Phe	TTG Leu	GAT Asp	CAT His	GAT Asp 340	AAA Lys	ACT Thr	CTT Leu	CAG Gln	ACT Thr 345	GAT Asp	TCT Ser	1179
ATA Ile	GAC Asp 350	AGT Ser	TTT Phe	GAA Glu	ACA Thr	CAG Gln	AGA Arg 355	ACA Thr	CCA Pro	CGA Arg	AAA Lys	AGT Ser 360	AAC Asn	CTT Leu	GAT Asp	1227
GAA Glu 365	GAG Glu	GTG Val	AAT Asn	GTA Val	ATT Ile 370	CCT Pro	CCA Pro	CAC His	ACT Thr	CCA Pro	GTT Val 375	AGG Arg	ACT Thr	GTT Val	ATG Met	1275
AAC Asn 380	ACT Thr	ATC Ile	CAA Gln	CAA Gln	TTA Leu 385	ATG Met	ATG Met	ATT Ile	TTA Leu	AAT Asn 390	TCA Ser	GCA Ala	AGT Ser	GAT Asp	CAA Gln 395	1323

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CCT	TCA	GAA	AAT	CTG	ATT	TCC	TAT	TTT	AAC	AAC	TGC	ACA	GTG	AAT	CCA	1371
Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	
				400					405					410		
AAA	GAA	AGT	ATA	CTG	AAA	AGA	GTG	AAG	GAT	ATA	GGA	TAC	ATC	TTT	AAA	1419
Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	
			415					420					425			
GAG	AAA	TTT	GCT	AAA	GCT	GTG	GGA	CAG	GGT	TGT	GTC	GAA	ATT	GGA	TCA	1467
Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	
			430				435					440				
CAG	CGA	TAC	AAA	CTT	GGA	GTT	CGC	TTG	TAT	TAC	CGA	GTA	ATG	GAA	TCC	1515
Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	
	445					450					455					
ATG	CTT	AAA	TCA	GAA	GAA	GAA	CGA	TTA	TCC	ATT	CAA	AAT	TTT	AGC	AAA	1563
Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	
460					465					470					475	
CTT	CTG	AAT	GAC	AAC	ATT	TTT	CAT	ATG	TCT	TTA	TTG	GCG	TGC	GCT	CTT	1611
Leu	Leu	Asn	Asp	Asn	Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	
				480					485					490		
GAG	GTT	GTA	ATG	GCC	ACA	TAT	AGC	AGA	AGT	ACA	TCT	CAG	AAT	CTT	GAT	1659
Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	
			495					500					505			
TCT	GGA	ACA	GAT	TTG	TCT	TTC	CCA	TGG	ATT	CTG	AAT	GTG	CTT	AAT	TTA	1707
Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	
		510					515					520				
AAA	GCC	TTT	GAT	TTT	TAC	AAA	GTG	ATC	GAA	AGT	TTT	ATC	AAA	GCA	GAA	1755
Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	
	525					530					535					
GGC	AAC	TTG	ACA	AGA	GAA	ATG	ATA	AAA	CAT	TTA	GAA	CGA	TGT	GAA	CAT	1803
Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	
540					545					550				555		
CGA	ATC	ATG	GAA	TCC	CTT	GCA	TGG	CTC	TCA	GAT	TCA	CCT	TTA	TTT	GAT	1851
Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	
				560					565					570		
CTT	ATT	AAA	CAA	TCA	AAG	GAC	CGA	GAA	GGA	CCA	ACT	GAT	CAC	CTT	GAA	1899
Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	
			575					580				585				
TCT	GCT	TGT	CCT	CTT	AAT	CTT	CCT	CTC	CAG	AAT	AAT	CAC	ACT	GCA	GCA	1947
Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	
		590					595					600				
GAT	ATG	TAT	CTT	TCT	CCT	GTA	AGA	TCT	CCA	AAG	AAA	AAA	GGT	TCA	ACT	1995
Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	
	605					610					615					
ACG	CGT	GTA	AAT	TCT	ACT	GCA	AAT	GCA	GAG	ACA	CAA	GCA	ACC	TCA	GCC	2043
Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	
620					625					630					635	
TTC	CAG	ACC	CAG	AAG	CCA	TTG	AAA	TCT	ACC	TCT	CTT	TCA	CTG	TTT	TAT	2091
Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	
				640					645					650		
AAA	AAA	GTG	TAT	CGG	CTA	GCC	TAT	CTC	CGG	CTA	AAT	ACA	CTT	TGT	GAA	2139
Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	
			655					660					665			

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CGC	CTT	CTG	TCT	GAG	CAC	CCA	GAA	TTA	GAA	CAT	ATC	ATC	TGG	ACC	CTT	2187
Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	
		670					675					680				
TTC	CAG	CAC	ACC	CTG	CAG	AAT	GAG	TAT	GAA	CTC	ATG	AGA	GAC	AGG	CAT	2235
Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	
	685					690					695					
TTG	GAC	CAA	ATT	ATG	ATG	TGT	TCC	ATG	TAT	GGC	ATA	TGC	AAA	GTG	AAG	2283
Leu	Asp	Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	
700					705					710					715	
AAT	ATA	GAC	CTT	AAA	TTC	AAA	ATC	ATT	GTA	ACA	GCA	TAC	AAG	GAT	CTT	2331
Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	
				720					725					730		
CCT	CAT	GCT	GTT	CAG	GAG	ACA	TTC	AAA	CGT	GTT	TTG	ATC	AAA	GAA	GAG	2379
Pro	His	Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	
			735					740					745			
GAG	TAT	GAT	TCT	ATT	ATA	GTA	TTC	TAT	AAC	TCG	GTC	TTC	ATG	CAG	AGA	2427
Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	
		750					755					760				
CTG	AAA	ACA	AAT	ATT	TTG	CAG	TAT	GCT	TCC	ACC	AGG	CCC	CCT	ACC	TTG	2475
Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	
	765					770					775					
TCA	CCA	ATA	CCT	CAC	ATT	CCT	CGA	AGC	CCT	TAC	AAG	TTT	CCT	AGT	TCA	2523
Ser	Pro	Ile	Pro	His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	
780					785					790					795	
CCC	TTA	CGG	ATT	CCT	GGA	GGG	AAC	ATC	TAT	ATT	TCA	CCC	CTG	AAG	AGT	2571
Pro	Leu	Arg	Ile	Pro	Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	
				800					805					810		
CCA	TAT	AAA	ATT	TCA	GAA	GGT	CTG	CCA	ACA	CCA	ACA	AAA	ATG	ACT	CCA	2619
Pro	Tyr	Lys	Ile	Ser	Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	
			815					820					825			
AGA	TCA	AGA	ATC	TTA	GTA	TCA	ATT	GGT	GAA	TCA	TTC	GGG	ACT	TCT	GAG	2667
Arg	Ser	Arg	Ile	Leu	Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	
		830					835					840				
AAG	TTC	CAG	AAA	ATA	AAT	CAG	ATG	GTA	TGT	AAC	AGC	GAC	CGT	GTG	CTC	2715
Lys	Phe	Gln	Lys	Ile	Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	
	845					850					855					
AAA	AGA	AGT	GCT	GAA	GGA	AGC	AAC	CCT	CCT	AAA	CCA	CTG	AAA	AAA	CTA	2763
Lys	Arg	Ser	Ala	Glu	Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	
860					865					870					875	
CGC	TTT	GAT	ATT	GAA	GGA	TCA	GAT	GAA	GCA	GAT	GGA	AGT	AAA	CAT	CTC	2811
Arg	Phe	Asp	Ile	Glu	Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	
				880					885					890		
CCA	GGA	GAG	TCC	AAA	TTT	CAG	CAG	AAA	CTG	GCA	GAA	ATG	ACT	TCT	ACT	2859
Pro	Gly	Glu	Ser	Lys	Phe	Gln	Gln	Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr	
			895					900					905			
CGA	ACA	CGA	ATG	CAA	AAG	CAG	AAA	ATG	AAT	GAT	AGC	ATG	GAT	ACC	TCA	2907
Arg	Thr	Arg	Met	Gln	Lys	Gln	Lys	Met	Asn	Asp	Ser	Met	Asp	Thr	Ser	
		910					915					920				

AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT 2962
 Asn Lys Glu Glu Lys
 925

GGATTCATTG TCTCTCACAG ATGTGACTGA TAT 2995

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	Ala	
1				5					10					15		
Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Glu	Asp	
			20					25					30			
Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu	Val	Arg	Leu	Glu	
		35					40					45				
Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu	
	50					55					60					
Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu	Thr	Trp	Glu	Lys	
65				70					75					80		
Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	Ile	Gln	Lys	Lys	Lys	
			85					90						95		
Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Asp	Glu	
			100					105					110			
Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	Val	
	115					120						125				
His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	Val	
	130				135						140					
Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala	
145				150						155				160		
Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln	
			165					170					175			
Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys	
			180					185					190			
Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met	
	195					200						205				
Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	
	210				215					220						
Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	
225				230					235					240		
Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	
			245					250						255		

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LA

Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser
610						615					620				
Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys
625					630					635					640
Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg
			645						650					655	
Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu
			660					665					670		
His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu
		675					680					685			
Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met
	690					695					700				
Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys
705					710					715					720
Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln
				725					730					735	
Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile
			740					745					750		
Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile
		755					760					765			
Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His
	770					775					780				
Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	Pro
785					790					795					800
Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	Ser
				805					810					815	
Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	Arg	Ile	Leu
			820					825					830		
Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	Gln	Lys	Ile
		835					840					845			
Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	Ser	Ala	Glu
	850					855					860				
Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	Asp	Ile	Glu
865					870					875					880
Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	Glu	Ser	Lys
				885					890					895	
Phe	Gln	Gln	Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr	Arg	Thr	Arg	Met	Gln
			900					905					910		
Lys	Gln	Lys	Met	Asn	Asp	Ser	Met	Asp	Thr	Ser	Asn	Lys	Glu	Glu	Lys
		915					920					925			

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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "Xaa = stop codon"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /note= "Xaa = stop codon"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 439
- (D) OTHER INFORMATION: /note= "Xaa = stop codon"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val	Xaa	Ser	His	Arg	Pro	Gly	Ser	Arg	Xaa	Leu	Leu	Gly	Ser	Gly	Asp	1	5	10	15
Thr	Leu	Arg	Ser	Gly	Trp	Glu	Arg	Ala	Phe	His	Asp	Gly	Asp	Thr	Leu	20	25	30	
Pro	Trp	Ile	Gly	Ser	Gln	Thr	Ala	Phe	Arg	Val	Thr	Ala	Met	Glu	Glu	35	40	45	
Pro	Gln	Ser	Asp	Pro	Ser	Val	Glu	Pro	Pro	Leu	Ser	Gln	Glu	Thr	Phe	50	55	60	
Ser	Asp	Leu	Trp	Lys	Leu	Leu	Pro	Glu	Asn	Asn	Val	Leu	Ser	Pro	Leu	65	70	75	80
Pro	Ser	Gln	Ala	Met	Asp	Asp	Leu	Met	Leu	Ser	Pro	Asp	Asp	Ile	Glu	85	90	95	
Gln	Trp	Phe	Thr	Glu	Asp	Pro	Gly	Pro	Asp	Glu	Ala	Pro	Arg	Met	Pro	100	105	110	
Glu	Ala	Ala	Pro	Pro	Val	Ala	Pro	Ala	Pro	Ala	Ala	Pro	Thr	Pro	Ala	115	120	125	
Ala	Pro	Ala	Pro	Ala	Pro	Ser	Trp	Pro	Leu	Ser	Ser	Ser	Val	Pro	Ser	130	135	140	
Gln	Lys	Thr	Tyr	Gln	Gly	Ser	Tyr	Gly	Phe	Arg	Leu	Gly	Phe	Leu	His	145	150	155	160
Ser	Gly	Thr	Ala	Lys	Ser	Val	Thr	Cys	Thr	Tyr	Ser	Pro	Ala	Leu	Asn	165	170	175	
Lys	Met	Phe	Cys	Gln	Leu	Ala	Lys	Thr	Cys	Pro	Val	Gln	Leu	Trp	Val	180	185	190	
Asp	Ser	Thr	Pro	Pro	Pro	Gly	Thr	Arg	Val	Arg	Ala	Met	Ala	Ile	Tyr	195	200	205	

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Lys	Gln	Ser	Gln	His	Met	Thr	Glu	Val	Val	Arg	Arg	Cys	Pro	His	His		
210						215					220						
Glu	Arg	Cys	Ser	Asp	Ser	Asp	Gly	Leu	Ala	Pro	Pro	Gln	His	Leu	Ile		
225					230					235					240		
Arg	Val	Glu	Gly	Asn	Leu	Arg	Val	Glu	Tyr	Leu	Asp	Asp	Arg	Asn	Thr		
				245					250					255			
Phe	Arg	His	Ser	Val	Val	Val	Pro	Tyr	Glu	Pro	Pro	Glu	Val	Gly	Ser		
			260					265					270				
Asp	Cys	Thr	Thr	Ile	His	Tyr	Asn	Tyr	Met	Cys	Asn	Ser	Ser	Cys	Met		
		275					280					285					
Gly	Gly	Met	Asn	Arg	Arg	Pro	Ile	Leu	Thr	Ile	Ile	Thr	Leu	Glu	Asp		
	290					295					300						
Ser	Ser	Gly	Asn	Leu	Leu	Gly	Arg	Asn	Ser	Phe	Glu	Val	Arg	Val	Cys		
305					310					315					320		
Ala	Cys	Pro	Gly	Arg	Asp	Arg	Arg	Thr	Glu	Glu	Glu	Asn	Leu	Arg	Lys		
				325					330					335			
Lys	Gly	Glu	Pro	His	His	Glu	Leu	Pro	Pro	Gly	Ser	Thr	Lys	Arg	Ala		
			340					345					350				
Leu	Pro	Asn	Asn	Thr	Ser	Ser	Ser	Pro	Gln	Pro	Lys	Lys	Lys	Pro	Leu		
		355					360					365					
Asp	Gly	Glu	Tyr	Phe	Thr	Leu	Gln	Ile	Arg	Gly	Arg	Glu	Arg	Phe	Glu		
	370					375					380						
Met	Phe	Arg	Glu	Leu	Asn	Glu	Ala	Leu	Glu	Leu	Lys	Asp	Ala	Gln	Ala		
385					390					395					400		
Gly	Lys	Glu	Pro	Gly	Gly	Ser	Arg	Ala	His	Ser	Ser	His	Leu	Lys	Ser		
				405					410					415			
Lys	Lys	Gly	Gln	Ser	Thr	Ser	Arg	His	Lys	Lys	Leu	Met	Phe	Lys	Thr		
			420					425					430				
Glu	Gly	Pro	Asp	Ser	Asp	Xaa											
		435															

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